

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/783,620
Source: TFW/6
Date Processed by STIC: 01/09/2007

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/783,620</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: <u>Unknown, Artificial Sequence, or scientific name (Genus/species).</u> <220>-<223> section is required when <213> response is <u>Unknown or is Artificial Sequence.</u> (see item 11 below)	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFW16

RAW SEQUENCE LISTING

DATE: 01/09/2007

PATENT APPLICATION: US/10/783,620

TIME: 12:53:55

Input Set : A:\14769US02.SEQ.txt

Output Set: N:\CRF4\01092007\J783620.raw

3 <110> APPLICANT: Jiang, Liwen
 4 SUN, Samuel Sai Ming
 6 <120> TITLE OF INVENTION: PLANT GENE EXPRESSION SYSTEM FOR PROCESSING, TARGETING AND
 7 ACCUMULATING FOREIGN PROTEINS IN TRANSGENIC SEEDS
 9 <130> FILE REFERENCE: 14769US02
 11 <140> CURRENT APPLICATION NUMBER: US 10/783,620
 12 <141> CURRENT FILING DATE: 2004-02-20
 14 <150> PRIOR APPLICATION NUMBER: US 60/449,367
 15 <151> PRIOR FILING DATE: 2003-02-21

17 <160> NUMBER OF SEQ ID NOS: 8
 19 <170> SOFTWARE: PatentIn version 3.3

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 32

23 <212> TYPE: PRT

24 <213> ORGANISM: cytoplasmic tail sequences from BP-80

26 <400> SEQUENCE: 1

28 Lys Tyr Arg Ile Arg Gln Tyr Met Asp Ser Glu Ile Arg Ala Ile Met

29 1 5 10 15

32 Ala Gln Tyr Met Pro Leu Asp Ser Gln Glu Glu Gly Pro Asn His Val

33 20 25 30

36 <210> SEQ ID NO: 2

37 <211> LENGTH: 22

38 <212> TYPE: PRT

39 <213> ORGANISM: cytoplasmic tail sequences from alpha-TIP

41 <400> SEQUENCE: 2

43 Lys Tyr Arg Ile Arg Pro Ile Glu Pro Pro Pro His His His Gln Pro

44 1 5 10 15

47 Leu Ala Thr Glu Asp Tyr

48 20

51 <210> SEQ ID NO: 3

52 <211> LENGTH: 16

53 <212> TYPE: PRT

54 <213> ORGANISM: FLAG epitope tag sequences operably linked to a spacer

57 <220> FEATURE:

58 <221> NAME/KEY: MISC_FEATURE

59 <222> LOCATION: (1)..(8)

60 <223> OTHER INFORMATION: FLAG epitope tag sequence

62 <220> FEATURE:

63 <221> NAME/KEY: MISC_FEATURE

64 <222> LOCATION: (9)..(16)

65 <223> OTHER INFORMATION: part of the luminal portion of BP-80 immediately adjacent to

the

66 TMD region

68 <400> SEQUENCE: 3

Does Not Comply
 Corrected Diskette Needed

CP8-1,2)
 Invalid Response.
 <213> Responses
 can be either
 Artificial,
 Unknown or
 Genes Specific
 see
 Item 10
 on Error
 Summary
 Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/783,620

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Input Set : A:\14769US02.SEQ.txt

Output Set: N:\CRF4\01092007\J783620.raw

70 Asp Tyr Lys Asp Asp Asp Asp Lys Ser Lys Thr Ala Ser Gln Ala Lys

71 1 5 10 15

74 <210> SEQ ID NO: 4

75 <211> LENGTH: 22

76 <212> TYPE: PRT

77 <213> ORGANISM: signal peptide sequences from proaleurain

79 <400> SEQUENCE: 4

81 Met Ala His Ala Arg Val Leu Leu Leu Ala Leu Ala Val Leu Ala Thr

82 1 5 10 15

85 Ala Ala Val Ala Val Ala

86 20

89 <210> SEQ ID NO: 5

90 <211> LENGTH: 23

91 <212> TYPE: PRT

92 <213> ORGANISM: transmembrane domain sequences from BP-80

94 <400> SEQUENCE: 5

96 Thr Trp Ala Ala Phe Trp Val Val Leu Ile Ala Leu Ala Met Ile Ala

97 1 5 10 15

100 Gly Gly Gly Phe Leu Val Tyr

101 20

104 <210> SEQ ID NO: 6

105 <211> LENGTH: 22

106 <212> TYPE: PRT

107 <213> ORGANISM: signal peptide sequences from the barley cysteine protease aleurain

109 <400> SEQUENCE: 6

111 Met Ala His Ala Arg Val Leu Leu Leu Ala Leu Ala Val Leu Ala Thr

112 1 5 10 15

115 Ala Ala Val Ala Val Ala

116 20

119 <210> SEQ ID NO: 7

120 <211> LENGTH: 24

121 <212> TYPE: PRT

122 <213> ORGANISM: signal peptide sequences from the rice storage protein glutelin

124 <400> SEQUENCE: 7

126 Met Ala Ser Ile Asn Arg Pro Ile Val Phe Phe Thr Val Cys Leu Phe

127 1 5 10 15

130 Leu Leu Cys Asp Gly Ser Leu Ala

131 20

134 <210> SEQ ID NO: 8

135 <211> LENGTH: 8

136 <212> TYPE: PRT

137 <213> ORGANISM: spacer

140 <220> FEATURE:

141 <221> NAME/KEY: MISC FEATURE

142 <223> OTHER INFORMATION: part of the luminal portion of BP-80 immediately adjacent to

the

143 TMD region

145 <400> SEQUENCE: 8

147 Ser Lys Thr Ala Ser Gln Ala Lys

148 1 5

7 Same Error

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/783,620

DATE: 01/09/2007

TIME: 12:53:56

Input Set : A:\14769US02.SEQ.txt

Output Set: N:\CRF4\01092007\J783620.raw